

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/516,558A
Source: PT
Date Processed by STIC: 3/9/06

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
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Revised 01/10/06



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006
TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

3 <110> APPLICANT: Chano, Tokuhiro
4 Okabe, Hidetoshi
5 Ikegawa, Shiro
7 <120> TITLE OF INVENTION: RB1 gene induced protein (RB1CC1) and gene
9 <130> FILE REFERENCE: 3190-070
11 <140> CURRENT APPLICATION NUMBER: US 10/516,558A
12 <141> CURRENT FILING DATE: 2004-11-30
14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00882
15 <151> PRIOR FILING DATE: 2003-01-30
17 <150> PRIOR APPLICATION NUMBER: JP P2002-161400
18 <151> PRIOR FILING DATE: 2002-06-03
20 <150> PRIOR APPLICATION NUMBER: JP P2002-214978
21 <151> PRIOR FILING DATE: 2002-07-24
23 <160> NUMBER OF SEQ ID NOS: 132
25 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1594
29 <212> TYPE: PRT
30 <213> ORGANISM: Unknown
32 <220> FEATURE:
33 <223> OTHER INFORMATION: human RB1CC1
35 <400> SEQUENCE: 1
37 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
38 1 5 10 15
41 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
42 20 25 30
45 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
46 35 40 45
49 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
50 50 55 60
53 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
54 65 70 75 80
E--> 57
58 Cys Asp Arg Pro Pro Ala Ile Pro Lys Thr Thr Phe Ser Thr Glu Asn
E--> 59 85 90 95
62 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
E--> 63 100 105 110
66 His Thr Val Ala Ser Arg Thr Gln Leu Ala Leu Glu Met Tyr Glu Val
E--> 67 115 120 125

*Does Not Comply
Corrected Diskette Needed*

*delete
page
number
→ (global
error)*

*Per 1.824 of
sequence rules,*

*no page numbers allowed
in
3/9/2006 computer
readable form*

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Input Set : A:\3190-070 Sequence Listing.txt

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70 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
 E--> 71 130 135 140
 74 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
 E--> 75 145 150 155 160
 78 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
 E--> 79 165 170 175
 82 Asn Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
 E--> 83 180 185 190
 86 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
 E--> 87 195 200 205
 90 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Leu Asp Ser Leu Pro
 E--> 91 210 215 220
 94 Glu His Glu Asp Ser Glu Lys Ala Glu Thr Lys Arg Ser Thr Glu Leu
 E--> 95 225 230 235 240
 98 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Glu Ser Leu Leu Thr
 E--> 99 245 250 255
 102 Ser Phe Pro Lys Ser Val Glu His Val Ser Pro Asp Thr Ala Asp Ala
 E--> 103 260 265 270
 106 Glu Ser Gly Lys Glu Ile Arg Glu Ser Cys Gln Ser Thr Val His Gln
 E--> 107 275 280 285
 110 Gln Asp Glu Thr Thr Ile Asp Thr Lys Asp Gly Asp Leu Pro Phe Phe
 E--> 111 290 295 300
 E--> 114 -2- *Delete ↙*
 116 Asn Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp
 E--> 117 305 310 315 320
 120 Val Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp
 E--> 121 325 330 335
 124 Pro Arg Ile Ile Arg Pro Phe Ile Ala Glu Cys Arg Gln Thr Ile Ala
 E--> 125 340 345 350
 128 Lys Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg
 E--> 129 355 360 365
 132 Leu Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Gly Arg Leu Val Asn
 E--> 133 370 375 380
 136 Glu Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Lys Arg Ala
 E--> 137 385 390 395 400
 140 Glu Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His
 E--> 141 405 410 415
 144 Ala Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp
 E--> 145 420 425 430
 148 Ile Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu
 E--> 149 435 440 445
 152 His Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln
 E--> 153 450 455 460
 156 Asp Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu
 E--> 157 465 470 475 480
 160 Glu Arg Val Lys Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr
 E--> 161 485 490 495
 164 Cys Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His
 E--> 165 500 505 510

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168 Tyr Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Arg Leu Tyr
 E--> 169 515 520 525
 E--> 171 -3-
 173 Glu Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys
 E--> 174 530 535 540
 177 Ser Phe Leu Arg Asn Arg Leu Phe Arg Gly Leu Asp Ser Trp Pro Pro
 E--> 178 545 550 555 560
 181 Ser Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp
 E--> 182 565 570 575
 185 Ile Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu
 E--> 186 580 585 590
 189 Val Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu
 E--> 190 595 600 605
 193 His Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser
 E--> 194 610 615 620
 197 Leu Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Ser Glu Gln Lys
 E--> 198 625 630 635 640
 201 Ala Ser Val Ser Gln Thr Ser Pro Gln Ser Ala Ser Ser Pro Arg Met
 E--> 202 645 650 655
 205 Glu Ser Thr Ala Gly Ile Thr Thr Thr Ser Pro Arg Thr Pro Pro
 E--> 206 660 665 670
 209 Pro Leu Thr Val Gln Asp Pro Leu Cys Pro Ala Val Cys Pro Leu Glu
 E--> 210 675 680 685
 213 Glu Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr
 E--> 214 690 695 700
 217 Ile Pro His Pro Asn Ile Glu Gln Thr Ile His Gln Val Ser Leu Asp
 E--> 218 705 710 715 720
 221 Leu Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val
 E--> 222 725 730 735
 225 Asn Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser
 E--> 226 740 745 750
 E--> 228 -4-
 229 Asp Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val
 E--> 230 755 760 765
 233 Ile Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Asn Val Cys Gly
 E--> 234 770 775 780
 237 Lys Glu Asp Phe Gly Asp His Thr Ser Leu Asn Val Gln Leu Glu Arg
 E--> 238 785 790 795 800
 241 Cys Arg Val Val Ala Gln Asp Ser His Phe Ser Ile Gln Thr Ile Lys
 E--> 242 805 810 815
 245 Glu Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp
 E--> 246 820 825 830
 249 Phe Ser Asn Ser Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile
 E--> 250 835 840 845
 253 Glu Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln
 E--> 254 850 855 860
 257 Lys Glu Leu Leu Ser Leu Lys Asn Glu Tyr Glu Gly Lys Leu Asp Gly
 E--> 258 865 870 875 880
 261 Leu Ile Lys Glu Thr Glu Glu Asn Glu Asn Lys Ile Lys Lys Leu Lys

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 nos.

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Input Set : A:\3190-070 Sequence Listing.txt

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E--> 262	885	890	895
265	Gly Glu Leu Val Cys Leu Glu Glu Val Leu Gln Asn Lys Asp Asn Glu		
E--> 266	900	905	910
269	Phe Ala Leu Val Lys His Glu Lys Glu Ala Val Ile Cys Leu Gln Asn		
E--> 270	915	920	925
273	Glu Lys Asp Gln Lys Leu Leu Glu Met Glu Asn Ile Met His Ser Gln		
E--> 274	930	935	940
277	Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile Val Leu Glu		
E--> 278	945	950	955
281	Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu Gln Leu Leu		
E--> 282	965	970	975
E--> 286		-5-	
287	Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys Glu Leu Glu		
E--> 288	980	985	990
291	Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys Val Met Thr		
E--> 292	995	1000	1005
295	Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn Gln Gln		
E--> 296	1010	1015	1020
299	Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln Glu		
E--> 300	1025	1030	1035
303	Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu		
E--> 304	1040	1045	1050
307	Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu		
E--> 308	1055	1060	1065
311	Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala		
E--> 312	1070	1075	1080
315	Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu		
E--> 316	1085	1090	1095
319	Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp		
E--> 320	1100	1105	1110
323	Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu		
E--> 324	1115	1120	1125
327	Met Thr Ile Glu Lys Asp Gln Arg Ile Ser Glu Leu Ile Ser Arg		
E--> 328	1130	1135	1140
331	His Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Val		
E--> 332	1145	1150	1155
335	Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Asn Leu Lys		
E--> 336	1160	1165	1170
339	Glu Gln Ile Ile Glu Leu Gln Ser Lys Leu Asp Ser Glu Leu Ser		
E--> 340	1175	1180	1185
E--> 343		-6-	
344	Ala Leu Glu Arg Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu		
E--> 345	1190	1195	1200
348	Lys Tyr Glu Ala Ile Ile Gln Asn Leu Glu Lys Asp Arg Gln Lys		
E--> 349	1205	1210	1215
352	Leu Val Ser Ser Gln Glu Gln Asp Arg Glu Gln Leu Ile Gln Lys		
E--> 353	1220	1225	1230
356	Leu Asn Cys Glu Lys Asp Glu Ala Ile Gln Thr Ala Leu Lys Glu		
E--> 357	1235	1240	1245

same
error

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Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

459 <210> SEQ ID NO: 2
 460 <211> LENGTH: 1588
 461 <212> TYPE: PRT
 462 <213> ORGANISM: Unknown
 464 <220> FEATURE:
 465 <223> OTHER INFORMATION: mouse Rb1cc1
 467 <400> SEQUENCE: 2

469 Met Lys Leu Tyr Val Phe Leu Val Asn Thr Gly Thr Thr Leu Thr Phe
 470 1 5 10 15
 473 Asp Thr Glu Leu Thr Val Gln Thr Val Ala Asp Leu Lys His Ala Ile
 474 20 25 30
 477 Gln Ser Lys Tyr Lys Ile Ala Ile Gln His Gln Val Leu Val Val Asn
 478 35 40 45
 481 Gly Gly Glu Cys Met Ala Ala Asp Arg Arg Val Cys Thr Tyr Ser Ala
 482 50 55 60
 485 Gly Thr Asp Thr Asn Pro Ile Phe Leu Phe Asn Lys Glu Met Ile Leu
 486 65 70 75 80
 489 Cys Asp Arg Ala Pro Ala Ile Pro Lys Ala Thr Phe Ser Thr Glu Asn
 490 85 90 95
 493 Asp Met Glu Ile Lys Val Glu Glu Ser Leu Met Met Pro Ala Val Phe
 494 100 105 110
 497 His Thr Val Ala Ser Arg Thr Gln Leu Ala Val Glu Met Tyr Asp Val
 498 115 120 125
 501 Ala Lys Lys Leu Cys Ser Phe Cys Glu Gly Leu Val His Asp Glu His
 502 130 135 140
 505 Leu Gln His Gln Gly Trp Ala Ala Ile Met Ala Asn Leu Glu Asp Cys
 506 145 150 155 160
 509 Ser Asn Ser Tyr Gln Lys Leu Leu Phe Lys Phe Glu Ser Ile Tyr Ser
 510 165 170 175
 513 Asp Tyr Leu Gln Ser Ile Glu Asp Ile Lys Leu Lys Leu Thr His Leu
 514 180 185 190
 E--> 515 -9- *delete*
 516 Gly Thr Ala Val Ser Val Met Ala Lys Ile Pro Leu Leu Glu Cys Leu
 E--> 517 195 200 205
 520 Thr Arg His Ser Tyr Arg Glu Cys Leu Gly Arg Pro Asp Ser Leu Asn
 E--> 521 210 215 220
 524 Glu His Glu Gly Ser Glu Lys Ala Glu Met Lys Arg Ser Thr Glu Leu
 E--> 525 225 230 235 240
 528 Val Leu Ser Pro Asp Met Pro Arg Thr Thr Asn Thr Ser Leu Val Thr
 E--> 529 245 250 255
 532 Ser Phe His Lys Ser Met Glu His Val Ala Pro Asp Pro Thr Gly Thr
 E--> 533 260 265 270
 536 Glu Arg Gly Lys Glu Leu Arg Glu Ser Cys Gln Ser Thr Val Gln Gln
 E--> 537 275 280 285
 540 Glu Glu Ala Ser Val Asp Ala Lys Asp Ser Asp Leu Pro Phe Phe Asn
 E--> 541 290 295 300
 544 Val Ser Leu Leu Asp Trp Ile Asn Val Gln Asp Arg Pro Asn Asp Val
 E--> 545 305 310 315 320
 548 Glu Ser Leu Val Arg Lys Cys Phe Asp Ser Met Ser Arg Leu Asp Pro

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647 Ser His Pro Asn Thr Glu Gln Pro Val His Gln Ala Ser Ile Asp Leu
 E--> 648 705 710 715 720
 651 Asp Ser Leu Ala Glu Ser Pro Glu Ser Asp Phe Met Ser Ala Val Asn
 E--> 652 725 730 735
 655 Glu Phe Val Ile Glu Glu Asn Leu Ser Ser Pro Asn Pro Ile Ser Asp
 E--> 656 740 745 750
 660 Pro Gln Ser Pro Glu Met Met Val Glu Ser Leu Tyr Ser Ser Val Ile
 E--> 661 755 760 765
 664 Asn Ala Ile Asp Ser Arg Arg Met Gln Asp Thr Ser Thr Arg Gly Asn
 E--> 665 770 775 780
 668 Glu Gly Phe Gly Asp Arg Ala Ala Leu His Val Gln Leu Glu Lys Cys
 E--> 669 785 790 795 800
 672 Arg Ala Ala Ala Gln Asp Ser His Thr Ser Ile Gln Thr Ile Lys Asp
 E--> 673 805 810 815
 676 Asp Leu Cys His Phe Arg Thr Phe Val Gln Lys Glu Gln Cys Asp Leu
 E--> 677 820 825 830
 680 Ala Asn Tyr Leu Lys Cys Thr Ala Val Glu Ile Arg Asn Ile Ile Glu
 E--> 681 835 840 845
 684 Lys Val Lys Cys Ser Leu Glu Ile Thr Leu Lys Glu Lys His Gln Gln
 E--> 685 850 855 860
 E--> 687 -12- *same*
 688 Glu Leu Gln Ser Leu Lys Ile Glu Tyr Cys Lys Leu Asp Ala Leu
 E--> 689 865 870 875 880
 692 Val Lys Asp Ser Glu Glu Asn Val Asn Lys Ile Leu Lys Leu Lys Glu
 E--> 693 885 890 895
 696 Asn Leu Val Ser Leu Glu Glu Ala Leu Gln Asn Lys Asp Asn Glu Phe
 E--> 697 900 905 910
 700 Thr Ser Ile Lys His Glu Lys Asp Ala Ile Val Cys Val Gln Gln Glu
 E--> 701 915 920 925
 705 Lys Asp Gln Lys Leu Leu Glu Met Glu Lys Ile Met His Thr Gln His
 E--> 706 930 935 940
 709 Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Met Ala Leu Glu Asp
 E--> 710 945 950 955 960
 713 Leu Lys Lys Leu His Asp Glu Lys Ile Glu Ser Leu Arg Ala Glu Phe
 E--> 714 965 970 975
 717 Gln Cys Leu Glu Glu Asn His Leu Lys Glu Leu Glu Asp Thr Leu His
 E--> 718 980 985 990
 721 Ile Arg His Thr Gln Glu Phe Glu Lys Val Met Thr Asp His Asn Met
 E--> 722 995 1000 1005
 725 Ser Leu Glu Lys Leu Lys Lys Glu Asn Gln Gln Arg Ile Asp Gln
 E--> 726 1010 1015 1020
 730 Met Leu Glu Ser His Ala Ser Thr Ile Gln Glu Lys Glu Gln Gln
 E--> 731 1025 1030 1035
 734 Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu Ser Asp Met Arg
 E--> 735 1040 1045 1050
 738 Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu Ala Glu Thr Asp
 E--> 739 1055 1060 1065
 742 Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Thr Gln Gln Lys Glu
 E--> 743 1070 1075 1080

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E--> 549 325 330 335
 552 Lys Ile Ile Gln Pro Phe Met Leu Glu Cys His Gln Thr Ile Ala Lys
 E--> 553 340 345 350
 556 Leu Asp Asn Gln Asn Met Lys Ala Ile Lys Gly Leu Glu Asp Arg Leu
 E--> 557 355 360 365
 560 Tyr Ala Leu Asp Gln Met Ile Ala Ser Cys Ser Arg Leu Val Asn Glu
 E--> 561 370 375 380
 564 Gln Lys Glu Leu Ala Gln Gly Phe Leu Ala Asn Gln Met Arg Ala Glu
 E--> 565 385 390 395 400
 568 Asn Leu Lys Asp Ala Ser Val Leu Pro Asp Leu Cys Leu Ser His Ala
 E--> 569 405 410 415
 E--> 572 410
 573 Asn Gln Leu Met Ile Met Leu Gln Asn His Arg Lys Leu Leu Asp Ile
 E--> 574 420 425 430
 577 Lys Gln Lys Cys Thr Thr Ala Lys Gln Glu Leu Ala Asn Asn Leu His
 E--> 578 435 440 445
 581 Val Arg Leu Lys Trp Cys Cys Phe Val Met Leu His Ala Asp Gln Asp
 E--> 582 450 455 460
 585 Gly Glu Lys Leu Gln Ala Leu Leu Arg Leu Val Ile Glu Leu Leu Glu
 E--> 586 465 470 475 480
 589 Arg Val Arg Ile Val Glu Ala Leu Ser Thr Val Pro Gln Met Tyr Cys
 E--> 590 485 490 495
 593 Leu Ala Val Val Glu Val Val Arg Arg Lys Met Phe Ile Lys His Tyr
 E--> 594 500 505 510
 597 Arg Glu Trp Ala Gly Ala Leu Val Lys Asp Gly Lys Gln Leu Tyr Glu
 E--> 598 515 520 525
 601 Ala Glu Lys Ser Lys Arg Glu Ser Phe Gly Lys Leu Phe Arg Lys Ser
 E--> 602 530 535 540
 605 Phe Leu Arg Asn Arg Leu Phe Lys Gly Leu Asp Ser Trp Pro Ser Ser
 E--> 606 545 550 555 560
 609 Phe Cys Thr Gln Lys Pro Arg Lys Phe Asp Cys Glu Leu Pro Asp Ile
 E--> 610 565 570 575
 613 Ser Leu Lys Asp Leu Gln Phe Leu Gln Ser Phe Cys Pro Ser Glu Val
 E--> 614 580 585 590
 617 Gln Pro Phe Leu Arg Val Pro Leu Leu Cys Asp Phe Glu Pro Leu His
 E--> 618 595 600 605
 621 Gln His Val Leu Ala Leu His Asn Leu Val Lys Ala Ala Gln Ser Leu
 E--> 622 610 615 620
 625 Asp Glu Met Ser Gln Thr Ile Thr Asp Leu Leu Asn Glu Gln Lys Val
 E--> 626 625 630 635 640
 E--> 628 630
 631 Ser Thr Ser Gln Ala Ser Pro Gln Ser Ala Ala Ser Pro Arg Ile Glu
 E--> 632 645 650 655
 635 Ser Thr Thr Gly Ile Thr Thr Thr Ser Pro Lys Thr Pro Pro Pro
 E--> 636 660 665 670
 639 Leu Thr Val Gln Asp Thr Leu Cys Pro Ala Val Cys Pro Leu Glu Glu
 E--> 640 675 680 685
 643 Leu Ser Pro Asp Ser Ile Asp Ala His Thr Phe Asp Phe Glu Thr Ile
 E--> 644 690 695 700

-11-

*Same
error*

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360	Phe	Lys	Leu	Glu	Arg	Glu	Val	Val	Glu	Lys	Glu	Leu	Glu	Lys	
E--> 361	1250						1255					1260			
364	Val	Lys	His	Leu	Glu	Asn	Gln	Ile	Ala	Lys	Ser	Pro	Ala	Ile	Asp
E--> 365	1265							1270					1275		
368	Ser	Thr	Arg	Gly	Asp	Ser	Ser	Ser	Leu	Val	Ala	Glu	Leu	Gln	Glu
E--> 369	1280							1285					1290		
372	Lys	Leu	Gln	Glu	Glu	Lys	Ala	Lys	Phe	Leu	Glu	Gln	Leu	Glu	Glu
E--> 373	1295							1300					1305		
376	Gln	Glu	Lys	Arg	Lys	Asn	Glu	Glu	Met	Gln	Asn	Val	Arg	Thr	Ser
E--> 377	1310							1315					1320		
380	Leu	Ile	Ala	Glu	Gln	Gln	Thr	Asn	Phe	Asn	Thr	Val	Leu	Thr	Arg
E--> 381	1325							1330					1335		
384	Glu	Lys	Met	Arg	Lys	Glu	Asn	Ile	Ile	Asn	Asp	Leu	Ser	Asp	Lys
E--> 385	1340							1345					1350		
388	Leu	Lys	Ser	Thr	Met	Gln	Gln	Gln	Glu	Arg	Asp	Lys	Asp	Leu	Ile
E--> 389	1355							1360					1365		
392	Glu	Ser	Leu	Ser	Glu	Asp	Arg	Ala	Arg	Leu	Leu	Glu	Glu	Lys	Lys
E--> 393	1370							1375					1380		
396	Lys	Leu	Glu	Glu	Glu	Val	Ser	Lys	Leu	Arg	Ser	Ser	Ser	Phe	Val
E--> 397	1385							1390					1395		
E--> 401														-7-	
402	Pro	Ser	Pro	Tyr	Val	Ala	Thr	Ala	Pro	Glu	Leu	Tyr	Gly	Ala	Cys
E--> 403	1400							1405					1410		
406	Ala	Pro	Glu	Leu	Pro	Gly	Glu	Ser	Asp	Arg	Ser	Ala	Val	Glu	Thr
E--> 407	1415							1420					1425		
410	Ala	Asp	Glu	Gly	Arg	Val	Asp	Ser	Ala	Met	Glu	Thr	Ser	Met	Met
E--> 411	1430							1435					1440		
414	Ser	Val	Gln	Glu	Asn	Ile	His	Met	Leu	Ser	Glu	Glu	Lys	Gln	Arg
E--> 415	1445							1450					1455		
418	Ile	Met	Leu	Leu	Glu	Arg	Thr	Leu	Gln	Leu	Lys	Glu	Glu	Glu	Asn
E--> 419	1460							1465					1470		
422	Lys	Arg	Leu	Asn	Gln	Arg	Leu	Met	Ser	Gln	Ser	Met	Ser	Ser	Val
E--> 423	1475							1480					1485		
426	Ser	Ser	Arg	His	Ser	Glu	Lys	Ile	Ala	Ile	Arg	Asp	Phe	Gln	Val
E--> 427	1490							1495					1500		
430	Gly	Asp	Leu	Val	Leu	Ile	Ile	Leu	Asp	Glu	Arg	His	Asp	Asn	Tyr
E--> 431	1505							1510					1515		
434	Val	Leu	Phe	Thr	Val	Ser	Pro	Thr	Leu	Tyr	Phe	Leu	His	Ser	Glu
E--> 435	1520							1525					1530		
438	Ser	Leu	Pro	Ala	Leu	Asp	Leu	Lys	Pro	Gly	Glu	Gly	Ala	Ser	Gly
E--> 439	1535							1540					1545		
442	Ala	Ser	Arg	Arg	Pro	Trp	Val	Leu	Gly	Lys	Val	Met	Glu	Lys	Glu
E--> 443	1550							1555					1560		
446	Tyr	Cys	Gln	Ala	Lys	Lys	Ala	Gln	Asn	Arg	Phe	Lys	Val	Pro	Leu
E--> 447	1565							1570					1575		
450	Gly	Thr	Lys	Phe	Tyr	Arg	Val	Lys	Ala	Val	Ser	Trp	Asn	Lys	Lys
E--> 451	1580							1585					1590		
454	Val														
E--> 458															

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006
TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

E--> 744

745 Met Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu Asn Leu Arg Thr
E--> 746 1085 1090 1095
749 Glu Ile Ser Lys Leu Asn Gln Lys Ile His Asp Asn Asn Glu Ser
E--> 750 1100 1105 1110
753 Tyr Gln Val Gly Leu Ser Glu Leu Arg Ala Leu Met Thr Ile Glu
E--> 754 1115 1120 1125
758 Lys Asp Gln Cys Ile Ser Glu Leu Ile Ser Arg His Glu Glu Glu
E--> 759 1130 1135 1140
762 Ser Asn Ile Leu Lys Ala Glu Leu Asp Asn Val Thr Ser Leu His
E--> 763 1145 1150 1155
766 Arg Gln Ala Tyr Glu Ile Glu Lys Lys Leu Lys Glu Gln Ile Val
E--> 767 1160 1165 1170
770 Glu Leu Gln Thr Arg Leu Asn Ser Glu Leu Ser Ala Leu Glu Lys
E--> 771 1175 1180 1185
774 Gln Lys Asp Glu Lys Ile Thr Gln Gln Glu Glu Lys Tyr Glu Ala
E--> 775 1190 1195 1200
778 Leu Ile Gln Asn Leu Glu Lys Asp Lys Glu Arg Leu Val Lys Asn
E--> 779 1205 1210 1215
782 His Glu Gln Asp Lys Glu His Leu Ile Gln Glu Leu Asn Phe Glu
E--> 783 1220 1225 1230
786 Lys Asn Lys Ala Val Gln Thr Ala Leu Asp Glu Phe Lys Val Glu
E--> 787 1235 1240 1245
790 Arg Glu Leu Val Glu Lys Glu Leu Leu Glu Lys Val Lys His Leu
E--> 791 1250 1255 1260
794 Glu Asn Gln Ile Ala Lys Thr Pro Ala Phe Glu Ser Ala Arg Glu
E--> 795 1265 1270 1275
798 Asp Ser Ser Ser Leu Val Ala Glu Leu Gln Glu Lys Leu Gln Glu
E--> 799 1280 1285 1290

E--> 802

803 Glu Lys Ala Lys Phe Leu Glu Gln Leu Glu Glu Gln Glu Lys Arg
E--> 804 1295 1300 1305
807 Lys Asn Glu Glu Met Gln Asn Val Arg Thr Ser Leu Ile Ala Glu
E--> 808 1310 1315 1320
811 Gln Gln Thr Asn Phe Asn Thr Val Leu Thr Arg Glu Lys Met Arg
E--> 812 1325 1330 1335
815 Lys Glu Asn Ile Ile Asn Asp Leu Ser Asp Lys Leu Lys Ser Thr
E--> 816 1340 1345 1350
819 Met Gln Gln Gln Glu Arg Asp Lys Asp Leu Ile Glu Ser Leu Ser
E--> 820 1355 1360 1365
823 Glu Asp Arg Ala Arg Leu Leu Glu Glu Lys Lys Gln Leu Glu Glu
E--> 824 1370 1375 1380
827 Glu Val Ser Lys Leu Arg Thr Ser Ser Phe Leu Ser Ser Ala Pro
E--> 828 1385 1390 1395
831 Val Ala Ala Ala Pro Glu Leu Tyr Gly Ala Cys Ala Pro Glu Leu
E--> 832 1400 1405 1410
835 Pro Gly Glu Pro Glu Arg Ser Val Met Glu Thr Ala Asp Glu Gly
E--> 836 1415 1420 1425
839 Arg Leu Asp Ser Ala Met Glu Thr Ser Met Met Ser Val Gln Glu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

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TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

E--> 840 1430 1435 1440
 843 Asn Met Leu Ser Glu Glu Lys Gln Arg Ile Met Leu Leu Glu Arg
 E--> 844 1445 1450 1455
 847 Thr Leu Gln Leu Lys Glu Glu Glu Asn Lys Arg Leu Asn Gln Arg
 E--> 848 1460 1465 1470
 851 Leu Met Ser Gln Ser Leu Ser Ser Val Ser Ser Arg His Ser Glu
 E--> 852 1475 1480 1485
 855 Lys Ile Ala Ile Arg Asp Phe Gln Val Gly Asp Leu Val Leu Ile
 E--> 856 1490 1495 1500
 E--> 858 -15- same
 861 Ile Leu Asp Glu Arg His Asp Asn Tyr Val Leu Phe Thr Val Ser
 E--> 862 1505 1510 1515
 865 Pro Thr Leu Tyr Phe Leu His Ser Glu Ser Leu Pro Ala Leu Asp
 E--> 866 1520 1525 1530
 868 Leu Lys Pro Gly Glu Gly Ala Ser Gly Ala Ser Arg Arg Pro Trp
 E--> 869 1535 1540 1545
 871 Val Leu Gly Lys Val Met Glu Lys Glu Tyr Cys Gln Ala Lys Lys
 E--> 872 1550 1555 1560
 875 Ala Gln Asn Arg Phe Lys Val Pro Leu Gly Thr Lys Phe Tyr Arg
 E--> 876 1565 1570 1575
 879 Val Lys Ala Val Ser Trp Asn Lys Lys Val
 E--> 880 1580 1585
 882 <210> SEQ ID NO: 3
 883 <211> LENGTH: 6636
 884 <212> TYPE: DNA
 885 <213> ORGANISM: Unknown
 887 <220> FEATURE:
 888 <223> OTHER INFORMATION: human RB1CC1 gene
 890 <400> SEQUENCE: 3
 891 gtcgacaata acaaaccagg ccggggcggt gtccggggcc ctggcgagcc ctggcggttg 60
 893 cctcagaatc ccccagtgcg ctggggccct cggctctgac agggccggc cttctgtccc 120
 895 cggccccag acccagagcc gagggggctg ctgcgcgtct tgccggcccg gacccttccc 180
 897 tgcctcctag agttcgggc cgcggcgccc gggcgcccg gacgcggcgt gttgtgtcgg 240
 899 cttacgggt ccgaatggc ggttggtaac cgctggcag gactaggcgg cggcggaaaga 300
 901 tgggccggg ggtcgctggc tctgctgctg ccgcggcga aggaggaggc gttggcggtt 360
 903 ttctgagtt aaccagtaat gccattcagt tgccaatctc aagcaaagca aacataagcc 420
 905 agtttaatc tacttttaa gaaaagtggt agtcctttc acagtgcctg acgttaactgt 480
 907 atcagagggt gaggtataag ctcacagaat tcagataat catcatgaag ttatatgtat 540
 909 ttctggtaa cactggaact actctaacat ttgacactga actttacagtg caaaactgtgg 600
 911 cagaccttaa gcatgccatt caaagcaa atcaagattgc tattcaacac caggtgctgg 660
 913 tggtaatgg aggagaatgc atggctgcag atcgatgtgtgttac agtgcgtggga 720
 E--> 915 -16- same
 918 cggataaaaa tccaaatttt ctttttaaca aagaaatgtat cttatgcgt cgtccacctg 780
 920 ctattcctaa aactaccctt tcgacagaaaa atgacatgga aataaaatgtt gaagaatctc 840
 922 ttatgtgcc tgcagtttt catactgttg cttcaaggac acagcttgcgat ttggaaatgt 900
 924 atgaagttgc caagaaactt tggctttt gtgaaggctc tgcatacatgtt gaacatctc 960
 926 aacaccaagg ctgggctgca atcatggcca acctggagga ctgttcaaat tcataccaaa 1020
 928 agctactttt caagttgaa agtattttt caaattatct gcagtccata gaagacatca 1080
 930 agttaaaaact tactcatttta ggaactgcag tttcagtaat ggccaagatt ccactgttgg 1140

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Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

932	agtgcctaac	cagacatagt	tacagagaat	gtttgggaag	actggattct	ttacctgaac	1200
934	atgaagactc	agaaaaagct	gagacgaaaa	gatccactga	actggtgctc	tctcctgata	1260
936	tgcctagaac	aactaacgaa	tctttgttaa	cctcatttcc	caagtcagt	gaacatgtgt	1320
938	cccgagatac	cgcagatgct	gaaagtggca	aagaaattag	ggaatcttgc	caaagtactg	1380
940	ttcatcagca	agatgaaact	acgattgaca	ctaaagatgg	tgatctgccc	ttttttaatg	1440
942	tctctttgtt	agactggata	aatgttcaag	atagacctaa	tgatgtggaa	tctttggtca	1500
944	ggaagtgctt	tgattctatg	acaggcctt	atccaaggat	tattcgacca	tttatacgag	1560
946	aatgccgtca	aactattgcc	aaacttgata	atcagaatat	gaaagccatt	aaaggacttg	1620
948	aagatcggt	ctacgcctg	gaccagatga	ttgcttagctg	tggccgactg	gtgaatgaac	1680
950	agaaagagct	tgctcaggga	tttttagcta	atcagaagag	agctgaaaac	ttaaaggatg	1740
952	catctgtatt	acctgattta	tgcctgagtc	acgcaaatca	gttcatgtatt	atgttgc当地	1800
954	atcatagaaa	actgttagat	attaagcaga	agtgtaccac	tgc当地acaa	gaactagcaa	1860
956	ataacctaca	tgtcagactg	aagtgggtt	gctttgtaat	gcttc当地gt	gatcaagatg	1920
958	gagagaagtt	acaagctt	ctccgcctg	taatagagct	gttagaaaga	gtcaaaaattg	1980
960	ttgaagctct	tagtacagtt	cctcagatgt	actgcttagc	tgttggtag	gttggtaagaa	2040
962	aaaaaatgtt	cataaaacac	tacagggagt	gggctgggtc	tttagtcaaa	gatggaaaga	2100
964	gattatatga	agcagaaaaaa	tcaaaaaggg	aatccttgg	aaaatttatt	aggaagtc当地	2160
966	tttaagaaa	tcgtctgtt	aggggactgg	actcctggcc	cccttc当地t	tgtactcaa	2220
968	agcctcgaaa	gtttgactgt	gaacttccag	atatttcatt	aaaagattt	cagtttctgc	2280
970	aatcatttt	tccttcggaa	gttcagccat	tcctcagggt	tcccttactt	tgtgacttt	2340
972	aacccttaca	ccagcatgta	cttgctctac	ataatttgg	aaaagcagca	caaagtttgg	2400

E--> 974

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975	ataaaaatgtc	acagaccatt	acagatctac	tgagtgaaca	aaaggcatct	gtgagccaga	2460
977	catccccaca	gtctgcttct	tcaccaagga	tggaaagtac	agcaggaatt	acaactacta	2520
979	cctcaccgag	aactcctcca	ccactgactg	ttcaggatcc	cttatgtcct	gcagttgtc	2580
981	ccttagaaga	attatctcca	gatagtattt	atgcacatac	gtttgatttt	gaaactattc	2640
983	cccatccaaa	catagaacag	actattcacc	aagtttctt	agacttggat	tcattagcag	2700
985	aaagtcttga	atcagatttt	atgtctgt	tgaatgagtt	tgtatagaaa	gaaaatttgt	2760
987	cgtctctaa	tcctataagt	gatccacaaa	gcccagaaat	gatggtgaa	tcactttt	2820
989	catcagttat	caatgcgata	gacagtagac	gaatgcagga	tacaaaatgt	tgtggtaagg	2880
991	aggattttgg	agatcatact	tctctgaatg	tccagttgg	aaagatgtaga	gttggtgccc	2940
993	aagactctca	cttcagttata	caaaccatta	aggaagacct	ttgccactt	agaacattt	3000
995	tacaaaaga	acagtgtgac	ttctcaatt	cattaaaatg	tacagcagta	gaaataagaa	3060
997	acattattga	aaaagtaaaa	tgttctctgg	aaataacact	aaaagaaaaaa	catcaaaaag	3120
999	aactactgtc	tttaaaaaat	gaatatgaag	gttaacttga	cggactaata	aggaaaactg	3180
1001	aagagaatga	aaacaaaatt	aaaaaattga	agggagagtt	agtatgc当地	gaggaggtt	3240
1003	tacaaaataa	agataatgaa	tttgctttgg	ttaaacatga	aaaagaagct	gtaatctgccc	3300
1005	tgcagaatga	aaaggatcag	aagtgttag	agatggaaaa	tataatgcac	tctcaaaaatt	3360
1007	gtgaaattaa	agaactgaag	cagtcacgag	aaatagtgtt	agaagactta	aaaaagctcc	3420
1009	atgtgaaaa	tgatgagaag	ttacagttat	tgagggcaga	acttc当地gt	ttggagcaaa	3480
1011	gtcatctaaa	ggaatttagag	gacacacttc	aggtttaggc	catacaagag	tttgagaagg	3540
1013	ttatgacaga	ccacagagtt	tctttggagg	aattaaaaaa	ggaaaatcaa	caaataatta	3600
1015	atcaaataca	agaatctcat	gctgaaattt	tccagggaaa	agaaaaacag	ttacaggaat	3660
1017	taaaactcaa	ggtttctgat	ttgtcagaca	cgagatgca	gttagaggtt	gaacttgc当地	3720
1019	tgaaggaagc	agaaaactgt	gaaataaaaa	tttgc当地gg	agaaagcaga	gcccagcaga	3780
1021	aggagacctt	gaaatctt	cttgc当地aa	agacagaaaa	tttgagaaca	gaaatttagt	3840
1023	aactcaacca	aaagattcag	gataataatg	aaaattatca	ggtgggctt	gcagagctaa	3900
1025	gaactttaat	gacaattgaa	aaagatcagc	gtatttccga	gttaatttagt	agacatgaag	3960
1027	aagaatctaa	tatacttaaa	gctgaattaa	acaaagtaac	atcttgc当地	aaccaagcat	4020

RAW SEQUENCE LISTING
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Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

1029	ttgaaaataga	aaaaaaccta	aaagaacaaa	taatttgaact	gcagagtaaa	ttggatttcag	4080
E--> 1031				-18-	Jane		
1032	aattttagtgc	tcttggaaaga	caaaaagatg	aaaaaattac	ccaaacaagaa	gagaatacgc	4140
1034	aagctattat	ccagaacctt	gagaaagaca	gacaaaaatt	ggtcagcgc	caggagcaag	4200
1036	acagagaaca	gttaatttcag	aagcttaatt	gtgaaaaaga	tgaagctatt	cagactgccc	4260
1038	taaaagaatt	taaatttggag	agagaagttg	ttgagaaaga	gttatttagaa	aaagttaaac	4320
1040	atcttgagaa	tcaaatacgca	aaaagtccctg	ccattgactc	taccagagga	gattcttcaa	4380
1042	gcttagttgc	tgaacttcaa	gaaaagcttc	aggaagaaaa	agctaagttt	ctagaacaac	4440
1044	ttgaagagca	agaaaaaaaaga	aagaatgaag	aaatgcaaaa	tgttgcgaca	tctttgttgc	4500
1046	cggaaacaaca	gccaatttt	aacactgttt	taacaagaga	gaaaatgaga	aaagaaaaca	4560
1048	taataaaatga	tcttagtgc	aagttgaaaa	gtacaatgca	gcaacaagaa	cgggataaaag	4620
1050	atttgataga	gtcactttct	gaagatcgag	ctcggttgc	tgagggaaaag	aaaaagcttg	4680
1052	aagaagaagt	cagtaagttg	cgcaagtagca	gttttgc	ttcaccat	gtagctacag	4740
1054	ccccagaact	ttatggagct	tgtgcacctg	aactccagg	tgaatcgat	agatccgctg	4800
1056	tggaaacagc	agatgaagga	agagtggatt	cagcaatgg	gacaagcatt	atgtctgtac	4860
1058	aagaaaatat	tcatatgtt	tctgaagaaa	aacagccgt	aatgtgtt	gaacgaacat	4920
1060	tgcaattgaa	agaagaagaa	aataaacgg	taaatcaaag	actgtatgt	cagagcatgt	4980
1062	cttcagtatc	ttcaaggcat	tctgaaaaaa	tagctattag	agattttcag	gtgggagatt	5040
1064	tggtaactcat	catcctagac	gaacgcccatt	acaattatgt	gttatttact	gttagtcata	5100
1066	ctttatattt	tctacattca	gagtcctc	ctgccc	tctcaaaacca	ggtgagggtg	5160
1068	cttcagggtgc	atctagaaga	ccctgggtac	ttggaaaagt	aatggaaaaa	gaataactgtc	5220
1070	aagccaaaaa	ggcacaaaac	agatttaaag	ttcc	tttgggg	gacaaagttt	5280
1072	aagccgtatc	atggataaag	aaagtataac	ttatggacaa	aattaataca	ttctatgaca	5340
1074	ttttttctg	atttgc	cagtgc	tcatcactc	aaaaacagca	ggccatctt	5400
1076	ttatgc	aaaa	gtcagcgt	caatatactt	cactgggt	catcg	5460
1078	gtttcatttt	aggaataata	aattcatcag	aatc	ccttggc	tgaattaaaa	5520
1080	tttttgc	tttttttac	ccagacaact	ctagaaatgc	ggaccaaact	acttcattt	5580
1082	ctcaaaggc	ataccttgc	cattgtggct	tatgtgagc	catattaatt	gcctgttaaa	5640
1084	tatacactag	cttgaactt	gatgtt	tttattttt	ccagcattt	tcctttgt	5700
1086	aaatcagtat	cagaataactt	gcacttta	acacatctt	tataaaatgt	ataaaattt	5760
E--> 1088				-19-			
1089	cagaactatt	taaaataaaag	aggagtgtt	ttgc	atcatttgc	tgagtttgc	5820
1091	tcagtagata	ctaaagcaaa	ttgtttc	atgtt	aaat	gttcaaaaa	5880
1093	aaaaaaaggaa	ctgtat	tttgc	tttgc	tttgc	atcagcaatc	5940
1095	ttcaaaagca	ctttc	atgttgc	tttgc	tttgc	ctgtgtact	6000
1097	aaccatttca	aatgc	caaa	tttgc	tttgc	aataatcata	6060
1099	tttgatgaaat	cgtaatttca	gttgc	tttgc	tttgc	gcacattaac	6120
1101	catttagagg	tcattttaa	aaacaaat	tgtat	tttgc	caattttaaa	6180
1103	acaataaaga	tttgc	aaatgtgt	tgc	tttgc	attttaata	6240
1105	tatttgatgt	attgttgc	agg	tatgtt	tatgtt	aagagaaaca	6300
1107	tgttatttac	aaaaatgtt	tttacttata	tactatgt	tatgtt	agtgatgt	6360
1109	agaatagaat	tgtgt	aaact	agatctt	tttgc	tttgc	6420
1111	tgtgttagtt	gagttggat	agaattgtt	tttgc	tttgc	tttgc	6480
1113	taatttcttt	tcagaaaata	tttatttct	tcataaaat	tttgc	tttgc	6540
1115	tatgtat	at	taatgtaca	aaatggata	tttgc	tttgc	6600
1117	acaagttat	gaataaaatg	acaaatgtt	tcaaa	tcaaa	tcaaa	6636
1120	<210>	SEQ	ID	NO:	4		
1121	<211>	LENGTH:	6518				
1122	<212>	TYPE:	DNA				

RAW SEQUENCE LISTING

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Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

1123 <213> ORGANISM: Unknown
 1125 <220> FEATURE:
 1126 <223> OTHER INFORMATION: mouse Rb1cc1 gene
 1128 <400> SEQUENCE: 4

1129 ccgagtcgac aataacaaac cccacggcgg ccgcgaccca gcccgtccaa gctctcagtg	60
1131 cctcgcccg cgactcggt tccccgcgcg gagccgaggg gccggagcag cggctgcgc	120
1133 cgaactccat cttccgggc ctgcgggggt actcgccggc tgggcgcgcg cgggtgtgtc	180
1135 ggttggcggc gccgcagggg cggtttagat ccgcgcgcg gcccaggcgc gccgcagaag	240
1137 atgggtcgga gggccgcgg ctgtgttgc gccgcggcgc gaggaggcgc tgccgggtct	300
1139 ctgagtttca ccagtaatgc cactcagttt ccaatatcaa gcaagcgcataaataagacaat	360
1141 tggtaatcttt taagaaaagt agtacttctc ttacatgtt ctggcggatc aacactggag	420
1143 ggtgaggtgt cagcttccag aaagatcatc atggatgtt atgtgtttct ggttaacacc	480
E--> 1145	-20- <i>some</i>
1146 ggaaccacgc tgacatttga cactgagctt actgtgcata ctgtggctga tcttaagcat	540
1148 gccattcaaa gcaaatacaa gattgttatt cagcaccagg ttctgggtgtt caatggagga	600
1150 gaatgtcatgg ctgcagatcg aagagtgtgt acttacagcg ctgggacggc cacaatcca	660
1152 atttttcttt ttaataaaga aatgtatctt tggatgtgtt cacatgttat tcctaaagct	720
1154 accctttcaa cagaaaatga catggaaataa aagtttgcg agtctttat gatccgtca	780
1156 gttttccaca ctgttgcctt aaggacacag ctgcgtgtt aatgtatgt cgttgcgaag	840
1158 aagctctgtcttcttctgtt aaggcttgcg catgtatgcg atcttcagca ccaaggctgg	900
1160 gctgcaatca tggccatctt ggaggactgt tcaattatcat accaaaaact tctttcaag	960
1162 tttgaaagta ttatcttgc ttatcttcaa tccatagaag acatcaagt aaaacttact	1020
1164 catttagaa ctgttgcctt agtataatggcc aagattccac tattggatgtt cctaaccaga	1080
1166 catagttaca gggaaatgtttt gggaaagaccg gattcttgcg atgaacatgcg aggttcagag	1140
1168 aaagctgaga tggaaatgttca tactgaaatgtt gtgtctctc ctgtatgttcc tagaacaacg	1200
1170 aacacatcct tggtaacctt atttccaaatg tcaatggcgtt atgtatgttcc agatcccacc	1260
1172 ggtactgaac gtggcaaaga actttagggaa tcttgcataa gtactgttca gcaagaagaa	1320
1174 gcttcgttgcg atgctaaaga cagtgtatctt ctttttttgcg atgtttctttt gtttagactgg	1380
1176 ataaatgttc aagatagacc caatgtatgtt gaatcttgcg tggatgttgc ttgttattct	1440
1178 atgagcggc ttgaccctt gattatttca ccattttatgt tagaatgttca tcaacttatt	1500
1180 gccaaacttgc ataatttgcgaa tatgaaagcc attaaaggcc ttgaaatgttcc gctgtatgtt	1560
1182 ttggaccaga tgattgttgcg ctgttgcgtt ctggtaatgtt aacagaaaaga gcttgcgttgc	1620
1184 ggatttttag ctaatcagat gagatgttgcg aacttgcgtt atgtatgttcc gttacacttgc	1680
1186 ctgtgtcttgc gtcgttgcgtt tcaacttgcg attatgttgcg aaaaaccacag aaaaacttgc	1740
1188 gatattaaac agaagtgcac cactgcgttgcg caagatgttgcg caaaacatctt ccacgttgc	1800
1190 ctgaagtgttgcg gtttttttgcg gatgtatgttgcg gtcgtatgttcc atggagaaaaa actgcggc	1860
1192 ctgttgcgttgcg ttgtatgttgcg gtcgtatgttgcg agatgttgcg ttgttgcgttgc tcttgcgttgc	1920
1194 gttcctcaga tggatgttgcg agtgttgcg gatgttgcg gtcgtatgttgcg ttgttgcgttgc	1980
1196 cactacagat agtgggtttgcg tggatgttgcg aacacatata tggatgttgcg ttgttgcgttgc	2040
1198 aagtcaaaaa gggaaatgttgcg tggatgttgcg ttgttgcgttgc gtcgtatgttgc tggatgttgc	2100
1200 tttaaaggac tggatgttgcg gtcgtatgttgcg ttgttgcgttgc gtcgtatgttgc tggatgttgc	2160
E--> 1202	-21-
1203 tggatgttgcg tggatgttgcg ttgttgcgttgc gtcgtatgttgc gtcgtatgttgc	2220
1205 gatattaaac agaagtgcac cactgcgttgcg caagatgttgcg caaaacatctt ccacgttgc	2280
1207 gatattaaac agaagtgcac cactgcgttgcg caagatgttgcg caaaacatctt ccacgttgc	2340
1209 attacatgttgcg tggatgttgcg gatgttgcg gtcgtatgttgc gtcgtatgttgc	2400
1211 gtcgtatgttgcg tggatgttgcg gatgttgcg gtcgtatgttgc gtcgtatgttgc	2460
1213 ctgttgcgttgcg ttgtatgttgcg gtcgtatgttgc gtcgtatgttgc tggatgttgc	2520
1215 ccagatgttgcg tggatgttgcg gtcgtatgttgc gtcgtatgttgc tggatgttgc	2580

RAW SEQUENCE LISTING

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Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

1217	caacctgttc	accaagcttc	tatagacttg	gattcattag	cagaaagccc	tgagtctgac	2640
1219	tttatgtctg	ctgtgaatga	gtttgtgata	gaagaaaatt	tatcgctcc	aaaccctata	2700
1221	agtatccac	aaagtccaga	aatgatggtg	gagtcacttt	actcttcagt	catcaatgca	2760
1223	atagatagta	ggcgtatgca	agacacaagt	acacgtggaa	acgagggcct	tggggatcg	2820
1225	gctgctctac	atgtccagct	ggagaaatgc	agagctgctg	cacaagactc	tcacaccagt	2880
1227	atacaaacca	tcaaggacga	tctgtccat	ttcagaacat	ttgtacaaaa	agaacagtgt	2940
1229	gacttagcaa	attattttaa	atgtacagct	gtagaaataa	gaaatattat	tgaaaaagta	3000
1231	aaatgttctc	tagaaataac	actaaaggaa	aagcatcagc	aagaactcca	atctttaaaa	3060
1233	attgagttatg	aatgtaaaact	tgatgctcta	gtaaaaagaca	gtgaagaaaa	tgtaaataaa	3120
1235	atttttaaaat	tgaaagaaaa	tttagtatcc	cttgaagagg	cttacaaaa	taaagacaat	3180
1237	gaattcactt	cgattaaaca	tgaaaaggat	gctattgtct	gtgtcagca	agaaaaggat	3240
1239	cagaagttgt	tagagatgga	aaagataatg	catactcaac	attgtgaaat	taaagaactg	3300
1241	aagcagtccac	gagagatggc	attagaagac	ctgaaaaagc	tgcatgatga	aaaaatcgag	3360
1243	tcattgagag	ctgaatttca	gtgcttagaa	gaaaatcacc	tgaaggaatt	agaggacaca	3420
1245	ctgcacatca	ggcacacaca	ggagtttgag	aaagttatga	cagaccacaa	tatgtctttg	3480
1247	gagaaattaa	aaaaagaaaa	ttagcaaaaga	attgaccaga	tgctagaatc	tcatgcctca	3540
1249	actattcagg	aaaaagagca	acagctgcag	gagttgaaac	tcaaagttc	tgacttgtca	3600
1251	gacatgagat	gtaagttaga	ggttgaactt	gcactaaagg	aagcagaaac	agatgagata	3660
1253	aagatcttgt	tggaaagagag	cagaacacag	cagaaggaaa	tgctgaagtc	tttacttgaa	3720
1255	caagagaccg	aaaacttaag	aacagaaaata	agtaaactaa	accaaaaaat	tcatgataat	3780
1257	aatgagagtt	accagggtgg	tttgcagag	ttaagagctt	taatgacaat	tgaaaaagat	3840
E--> 1259							

-22-

some

1260	cagtgcattt	cagagttaat	cagtagacat	gaagaagaat	ctaataatact	taaggctgaa	3900
1262	ttagacaatg	ttacatctt	gcatgccaa	gcatatgaaa	tagaaaaaaa	actgaaagaa	3960
1264	caaatagttg	aattgcagac	tagattgaac	tcagaattga	tgctcttga	aaaacagaaa	4020
1266	gatgaaaaaa	ttacccaaca	agaagagaag	tatgaagcac	ttatccagaa	ccttgagaaa	4080
1268	gacaaggaga	gactggcaa	gaaccacgag	caagacaaag	aacacttaat	tcaggagctt	4140
1270	aattttgaaa	aaaacaaaagc	tgttcaaact	gcactagatg	aatttaaggt	ggagagagaa	4200
1272	cttgcggaaa	aagagttatt	agaaaaagg	aaacatctt	agaatcaa	agccaaaact	4260
1274	cctgcctttg	agtcaagccag	agaagattt	tcaagcttag	ttgcggaaact	tcaagagaaa	4320
1276	cttcaagaag	aaaagctaa	gtttctggaa	caacttgaag	aacaagagaa	aagaaaagaat	4380
1278	gaggaaatgc	aaaatgtcag	aacctcttt	attgctgagc	agcagaccaa	ctttaacaca	4440
1280	gtcttaacaa	gagagaaaat	gaggaaagaa	aacataataa	atgatcttag	tgataagcta	4500
1282	aaaagtacaa	tgcagcagca	agagcgggat	aaagattga	tagagtcgt	ctctgaggac	4560
1284	cgagctcggt	tgcttgaaga	gaagaagcag	tttgaagagg	aagttagtta	actccgcact	4620
1286	acagttttc	tttcctcagc	acctgtggct	gcagccccag	agctctatgg	tgctgtgc	4680
1288	cctgagctcc	caggggagcc	agagagatca	gtcatggaga	cggcagatga	aggaagactg	4740
1290	gattccgcaa	tggagacaag	catgatgtct	gtccaaagaaa	acatgttatac	tgaagagaag	4800
1292	cagaggatca	tgctcttaga	acggacattt	cagttgaaag	aagaagaaaa	caagcggtta	4860
1294	aatcaaagac	tgtatgtctca	gagtttgcct	tcaatgtctt	caaggcattc	tgaaaaataa	4920
1296	gccatttagag	attttcaggt	gggagattt	gttctcatca	tccttagatga	gcggcacgac	4980
1298	aattatgtat	tgtttactgt	tagtcctact	ttatattttc	tgcactcaga	gtctttcct	5040
1300	gccttggatc	tcaaaccagg	tgagggagct	tcaggtgc	ctagaagacc	ctgggtcctt	5100
1302	gggaaaagtaa	tggaaaagga	atactgtcaa	gccaaaaagg	cacaaaacag	atttaaagtt	5160
1304	cctttgggaa	caaagttta	cagagtggaa	gctgtgtcat	ggaataagaa	agtatagcca	5220
1306	cagaagaaat	ctctacatct	cataccattt	ttgatttgc	ctccagtgt	gataaaactac	5280
1308	tctaaaaaca	gctggccatt	gttgggtttt	tttttgtt	ttgtttgtt	gtttgtttt	5340
1310	acaaaaagtca	acataacaat	atacttcatt	ggtggactgc	acttacctt	taagtggcta	5400
1312	catcttagga	acaataaatt	tattaaaatt	cttggctgaa	tcaaaatgg	tttggttt	5460

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:13

Input Set : A:\3190-070 Sequence Listing.txt

Output Set: N:\CRF4\03092006\J516558A.raw

1314 ttccacccaa ataactagaa attcggacca aaatagatgt tttccaaggg cagagcctgc 5520
E--> 1316 -23- *yr 24-25 also appear (but not shown on this page)*
 1317 actgtggctt gtgactagcc tcattagttt cctgttaata aacattagct gaatagttac 5580
 1319 cagtgtgtt accagcattt gtccttctgt gaattcaaga gtcctcgac tctttaacat 5640
 1321 gttcttata aaatgtataa acccttccaa actattaaa gaggagtgtt attgcatgca 5700
 1323 gataatcata atttttagtt tgcctcagaa gactactaaa gcaaatttgc tcatttttt 5760
 1325 ttaaaaaaaat gcccttaat gttcaaaaaa aaaataacag tctaatttga ctgactttaa 5820
 1327 gatcagccat aaataatgag cagtcttcaa aagcactttt cacacagatc atctgggctc 5880
 1329 cagggaggaa gagtcgtgc cactgatgtt ttcaagtgc ggactcactc aaacctctca 5940
 1331 gcatcttagg actgtttcaa gtaatcatat tcatgtactc gtaattcatg gttgaccttc 6000
 1333 agaagaagat attcattgtt tattaacatt tagaggtcat taaaataaca aaagtctgt 6060
 1335 ttgtaaagga cctgtacaat ttaagacaaa taaagaattt aaagtgtaaa tttgtgtgcc 6120
 1337 ttttaaaggat tacattttaa atatattgcg tgatttctgg gaaaggtgaa aaaaatgttc 6180
 1339 tttatcaaaag agaaacctgt ttataaaaaa atgttgcattt tttcctatgt aacagggtga 6240
 1341 agtgggttgc tttggaaacag aaccatgtt actcaagggtt taaaagctgg cactgaacaa 6300
 1343 agatattgaa gtatcttaggc tagttgattt gaaagagttt cttcagggtt gttgttagca 6360
 1345 gtaataatg attcttttc agaaatattt aatttctcca taaaataaaatg ttggatattt 6420
 1347 ttataaatat gtaatctaat agaatgaaaaa tggataaaac atagtgtata gaatacctaa 6480
 1349 ttcaaaaaca tattaatgaa taaacgaaca aatgatta 6518

1475 <210> SEQ ID NO: 15
 1476 <211> LENGTH: 21
 1477 <212> TYPE: DNA
 1478 <213> ORGANISM: Artificial
 1480 <220> FEATURE:
 1481 <223> OTHER INFORMATION: artificially synthesized primer sequence called

CC1-S8

1483 <400> SEQUENCE: 15
 1484 aaggaagacc tttgccactt t
E--> 1487 -26- *also yr 27-28*
 1645 <210> SEQ ID NO: 29
 1646 <211> LENGTH: 20
 1647 <212> TYPE: DNA
 1648 <213> ORGANISM: Artificial
 1650 <220> FEATURE:
 1651 <223> OTHER INFORMATION: artificially synthesized primer sequence called

RB1CC-R3

1653 <400> SEQUENCE: 29
 1654 aaactcagaa aaccggcaac
E--> 1657 -29- *also 30-31*
 1818 <210> SEQ ID NO: 43
 1819 <211> LENGTH: 20
 1820 <212> TYPE: DNA
 1821 <213> ORGANISM: Artificial
 1823 <220> FEATURE:
 1824 <223> OTHER INFORMATION: artificially synthesized primer sequence called

MMK1-2-S

1826 <400> SEQUENCE: 43
 1827 taagcatgcc attcaaagca
E--> 1830 -32- *also 30-31*
 1990 <210> SEQ ID NO: 57
 1991 <211> LENGTH: 20
 1992 <212> TYPE: DNA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006
TIME: 12:25:14

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

1993 <213> ORGANISM: Artificial
1995 <220> FEATURE:
1996 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MCC-S8
1998 <400> SEQUENCE: 57
1999 acgtggcaaa gaacttaggg
E--> 2003
2161 <210> SEQ ID NO: 71
2162 <211> LENGTH: 20
2163 <212> TYPE: DNA
2164 <213> ORGANISM: Artificial
2166 <220> FEATURE:
2167 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MCC-AS3
2169 <400> SEQUENCE: 71
2170 tgccgctcat ctaggatgat
E--> 2174
2394 <210> SEQ ID NO: 90
2395 <211> LENGTH: 20
2396 <212> TYPE: DNA
2397 <213> ORGANISM: Artificial
2399 <220> FEATURE:
2400 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MINT2-S0
2402 <400> SEQUENCE: 90
2403 tgccactcag ttgccaagta
E--> 2404
2564 <210> SEQ ID NO: 104
2565 <211> LENGTH: 20
2566 <212> TYPE: DNA
2567 <213> ORGANISM: Artificial
2569 <220> FEATURE:
2570 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MINT9-AS
2572 <400> SEQUENCE: 104
2573 gcctgcagtt tttctccatc
E--> 2576
2738 <210> SEQ ID NO: 118
2739 <211> LENGTH: 20
2740 <212> TYPE: DNA
2741 <213> ORGANISM: Artificial
2743 <220> FEATURE:
2744 <223> OTHER INFORMATION: artificially synthesized primer sequence called
MINT16-AS
2746 <400> SEQUENCE: 118
2747 gctcttgctg ctgcattgt
E--> 2751
2910 <210> SEQ ID NO: 132
2911 <211> LENGTH: 20
2912 <212> TYPE: DNA
2913 <213> ORGANISM: Artificial
2915 <220> FEATURE:
2916 <223> OTHER INFORMATION: artificially synthesized primer sequence called

-35-

also 33-34

20

-38-

also 36-37

20

-42-

also 39-41

20

-45-

also 42-44

20

primer

-48-

also 45-47

20

Sequence

sequence

MINT23-AS
2918 <400> SEQUENCE: 132

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006

TIME: 12:25:14

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

2919 cagcactgga ggacaaatca
E--> 2922

20

-51-

also 49-50

19
VERIFICATION SUMMARY
PATENT APPLICATION: US/10/516,558A

DATE: 03/09/2006
TIME: 12:25:15

Input Set : A:\3190-070 Sequence Listing.txt
Output Set: N:\CRF4\03092006\J516558A.raw

L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:515 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:915 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=3
L:1145 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=4
L:1374 M:283 W: Missing Blank Line separator, <400> field identifier
L:1430 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1487 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:1545 M:283 W: Missing Blank Line separator, <400> field identifier
L:1601 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1602 M:283 W: Missing Blank Line separator, <220> field identifier
L:1657 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:1717 M:283 W: Missing Blank Line separator, <400> field identifier
L:1773 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:1774 M:283 W: Missing Blank Line separator, <220> field identifier
L:1830 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:1888 M:283 W: Missing Blank Line separator, <400> field identifier
L:1945 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2003 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2061 M:283 W: Missing Blank Line separator, <400> field identifier
L:2117 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2118 M:283 W: Missing Blank Line separator, <220> field identifier
L:2174 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2232 M:283 W: Missing Blank Line separator, <400> field identifier
L:2290 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2291 M:283 W: Missing Blank Line separator, <220> field identifier
L:2347 M:259 W: Allowed number of lines exceeded, <211> LENGTH:
L:2404 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2518 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2519 M:283 W: Missing Blank Line separator, <220> field identifier
L:2576 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2638 M:283 W: Missing Blank Line separator, <400> field identifier
L:2694 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2695 M:283 W: Missing Blank Line separator, <220> field identifier
L:2751 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:2809 M:283 W: Missing Blank Line separator, <400> field identifier
L:2865 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:2866 M:283 W: Missing Blank Line separator, <220> field identifier
L:2922 M:254 E: No. of Bases conflict, this line has no nucleotides.